#2 01PE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/823,676

DATE: 04/18/2001 TIME: 07:58:18

Input Set : A:\MBI0034 sequence listing.txt
Output Set: N:\CRF3\04182001\I823676.raw

ENTERED

<pre>3 <110> APPLICANT: Jiang, Cai-Zhong 5 <120> TITLE OF INVENTION: Method for Modifyin</pre>	g Plant Biomass
7 <130> FILE REFERENCE: MBI-0034 C> 9 <140> CURRENT APPLICATION NUMBER, US (09 (923 6	
C> 9 <140> CURRENT APPLICATION NUMBER: US/09/823,6 C> 9 <141> CURRENT FILING DATE: 2001-03-30	76
9 <160> NUMBER OF SEQ ID NOS: 8	
11 <170> SOFTWARE: PatentIn version 3.0	
13 <210> SEQ ID NO: 1	
14 <211> LENGTH: 974	
15 <212> TYPE: DNA	
16 <213> ORGANISM: Arabidopsis thaliana	
18 <220> FEATURE:	
19 <221> NAME/KEY: CDS 20 <222> LOCATION: (62)(874)	
21 <223> OTHER INFORMATION: G1073	
24 <400> SEQUENCE: 1	
25 ccccccgacc tgcctctaca gagacctgaa gattccagaa c	cccacctga tcaaaaataa 60
27 c atg gaa ctt aac aga tct gaa gca gac gaa gca	aag gcc gag acc act 109
28 Met Glu Leu Asn Arg Ser Glu Ala Asp Glu Ala	Lys Ala Glu Thr Thr
29 1 5 10	15
31 ccc acc ggt gga gcc acc agc tca gcc aca gcc tc	et gge tet tee tee 157
32 Pro Thr Gly Gly Ala Thr Ser Ser Ala Thr Ala Se 33 20 25	
35 gga cgt cgt cca cgt ggt cgt cct gca ggt tcc aa	30 aa aac aaa ccc aaa 205
36 Gly Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Ly	rs Asn Lus Pro Lus
37 35 40	45
39 cct ccg acg att ata act aga gat agt cct aac gt	c ctt aga tca cac 253
40 Pro Pro Thr Ile Ile Thr Arg Asp Ser Pro Asn Va	l Leu Arg Ser His
41 50 55 60	
43 gtt ctt gaa gtc acc tcc ggt tcg gac ata tcc ga	g gca gtc tcc acc 301
44 Val Leu Glu Val Thr Ser Gly Ser Asp Ile Ser Gl 45 65 70 75	
47 tac gcc act cgt cgc ggc tgc ggc gtt tgc att at	80
48 Tyr Ala Thr Arg Arg Gly Cys Gly Val Cys Ile Il	a agc ggc acg ggt 349
49 85 90	95
51 gcg gtc act aac gtc acg ata cgg caa cct gcg gc	t ccq qct qqt qqa 397
52 Ala Val Thr Asn Val Thr Ile Arg Gln Pro Ala Al	a Pro Ala Gly Gly
53 100 105	110
55 ggt gtg att acc ctg cat ggt cgg ttt gac att tt	g tot ttg acc ggt 445
56 Gly Val Ile Thr Leu His Gly Arg Phe Asp Ile Le 57 115 120	
57 115 120 59 act gcg ctt cca ccg cct gca cca ccg gga gca gg	125
60 Thr Ala Leu Pro Pro Pro Ala Pro Pro Gly Ala Gl	a ggt ttg acg gtg 493
61 130 135 14	
63 tat cta gcc gga ggt caa gga caa gtt gta gga gg	g aat gtg gct ggt 541
64 Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gl	y Asn Val Ala Gly
65 145 150 155	160

RAW SEQUENCE LISTING DATE: 04/18/2001 PATENT APPLICATION: US/09/823,676 TIME: 07:58:18

Input Set : A:\MBI0034 sequence listing.txt
Output Set: N:\CRF3\04182001\I823676.raw

	tcg Ser			_	_		_	_		_	-	-	_			-	589
71	aac Asn	-	-		gat			_		gaa		-	-		cca	_	637
75	ccg Pro			acc				-	cag	-	-		-	tct	_	_	685
	tcg Ser																733
84	ggt Gly 225							_	_						_		781
	atg Met																829
91	ggt Gly	_			ggt					act	-						874
95 97 100	gcta <21	ctag 0> S	ct a EQ I	tttg tage D NO	ggtt : 2				gcg			gttt	gacc		iaact	actag	934 974
T01	. <21	T> P	ENGT	H: 2	70												
102 103	<21 <21	2> T 3> O	YPE:	PRT	Ara	bido	psis	tha	lian	a							
102 103 105 107 108	<21 <21 <40 Met 1	2> T 3> O 0> S Glu	YPE: RGAN EQUE Leu	PRT ISM: NCE: Asn	Ara 2 Arg 5	Ser	Glu	. Ala	Asp	Glu 10		_			15	Thr	
102 103 105 107 108 111 112	<21 <21 <40 Met 1 Pro	2> T 3> 0 0> S Glu Thr	YPE: RGAN EQUE Leu Gly	PRT ISM: NCE: Asn Gly 20	Ara 2 Arg 5 Ala	Ser Thr	Glu Ser	Ala Ser	Asp Ala 25	Glu 10 Thr	Ala	Ser	Gly	Ser	15 Ser	Ser	
102 103 105 107 108 111 112 115	<21 <21 <40 Met 1 Pro	2> T 3> O 0> S Glu Thr	YPE: RGAN EQUE Leu Gly Arg 35	PRT ISM: NCE: Asn Gly 20 Pro	Ara 2 Arg 5 Ala Arg	Ser Thr	Glu Ser Arg	Ser Pro	Asp Ala 25 Ala	Glu 10 Thr	Ala Ser	Ser	Gly Asn 45	Ser 30 Lys	15 Ser		
102 103 105 107 108 111 112 115 116 119 120	<21 <21 <40 Met 1 Pro Gly Pro Val	2> T 3> O 0> S Glu Thr Arg Pro 50	YPE: RGAN EQUE Leu Gly Arg 35 Thr	PRT ISM: NCE: Asn Gly 20 Pro	Ara 2 Arg 5 Ala Arg	Ser Thr Gly Thr	Glu Ser Arg Arg	Ser Pro 40 Asp	Asp Ala 25 Ala Ser	Glu 10 Thr Gly Pro	Ala Ser Asn Ser	Ser Lys Val 60	Asn 45 Leu	Ser 30 Lys	15 Ser Pro	Ser Lys His	
102 103 105 107 108 111 112 115 116 119 120 123	<21 <40 Met 1 Pro Gly Pro Val 65 Tyr	2> T 3> O 0> S Glu Thr Arg Pro 50 Leu	YPE: RGAN EQUE Leu Gly Arg 35 Thr	PRT ISM: NCE: Asn Gly 20 Pro Ile	Ara 2 Arg 5 Ala Arg Ile	Ser Thr Gly Thr Ser 70	Ser Arg Arg 55 Gly	Ser Pro 40 Asp	Asp Ala 25 Ala Ser Asp	Glu 10 Thr Gly Pro	Ala Ser Asn Ser 75	Ser Lys Val 60 Glu	Gly Asn 45 Leu	Ser 30 Lys Arg	15 Ser Pro	Ser Lys	
102 103 105 107 108 111 112 115 116 119 120 123 124 127 128 131 132	<21 <21 <40 Met 1 Pro Gly Pro Val 65 Tyr Ala	2> T 3> O 0> S Glu Thr Arg Pro 50 Leu Ala	YPE: RGAN EQUE Leu Gly Arg 35 Thr Glu Thr	PRTISM: ISM: Asn Gly 20 Pro Ile Val Arg Asn 100	Ara 2 Arg 5 Ala Arg Ile Thr Arg 85 Val	Ser Thr Gly Thr Ser 70 Gly	Ser Arg Arg 55 Gly Cys	Ala Ser Pro 40 Asp Ser Gly	Asp Ala 25 Ala Ser Asp Val Gln 105	Glu 10 Thr Gly Pro Ile Cys 90 Pro	Ala Ser Asn Ser 75 Ile Ala	Ser Lys Val 60 Glu Ile	Gly Asn 45 Leu Ala Ser	Ser 30 Lys Arg Val Gly Ala 110	15 Ser Pro Ser Ser Thr 95 Gly	E Ser Lys His Thr 80 Gly	
102 103 105 107 108 111 112 115 116 119 120 123 124 127 128 131 132 135 136	<21 <40 Met 1 Pro Gly Pro Val 65 Tyr Ala Gly	2> T 3> O 0> S Glu Thr Arg Pro 50 Leu Ala Val	YPE: RGAN EQUE Leu Gly Arg 35 Thr Glu Thr Thr	PRT ISM: ISM: NCE: Asn Gly 20 Pro Ile Val Arg Asn 100 Thr	Ara 2 Arg 5 Ala Arg Ile Thr Arg 85 Val	Thr Gly Thr Ser 70 Gly Thr	Ser Arg Arg 55 Gly Cys Ile	Ala Ser Pro 40 Asp Ser Gly Arg Arg	Asp Ala 25 Ala Ser Asp Val Gln 105 Phe	Glu 10 Thr Gly Pro Ile Cys 90 Pro	Ala Ser Asn Ser 75 Ile Ala Ile	Ser Lys Val 60 Glu Ile Ala	Asn 45 Leu Ala Ser Pro	Ser 30 Lys Arg Val Gly Ala 110 Leu	15 Ser Pro Ser Ser Thr 95 Gly	E Ser Lys His Thr 80 Gly Gly	
102 103 105 107 108 111 112 115 116 129 123 124 127 128 131 132 135 136 139 140 143	<21 <21 <40 Met 1 Pro Gly Pro Val 65 Tyr Ala Gly Thr	2> T 3> O 0> S Glu Thr Arg Pro 50 Leu Ala Val Val Ala 130	YPE: RGAN EQUE Leu Gly Arg 35 Thr Glu Thr Thr Ile 115 Leu	PRT ISM: INCE: Asn Gly 20 Pro Ile Val Arg Asn 100 Thr	Ara 2 Arg 5 Ala Arg Ile Thr Arg 85 Val Leu Pro	Thr Gly Thr Ser 70 Gly Thr His	Ser Arg 55 Gly Cys Ile Gly Ala 135	Ala Ser 40 Asp Ser Gly Arg 120 Pro	Asp Ala 25 Ala Ser Asp Val Gln 105 Phe	Glu 10 Thr Gly Pro Ile Cys 90 Pro Asp	Ala Ser Asn Ser 75 Ile Ala Ile	Ser Lys Val 60 Glu Ile Ala Leu Gly 140	Asn 45 Leu Ala Ser Pro Ser 125 Gly	Ser 30 Lys Arg Val Gly Ala 110 Leu	15 Ser Pro Ser Ser Thr 95 Gly Thr	E Ser Lys His Thr 80 Gly	

RAW SEQUENCE LISTING DATE: 04/18/2001 PATENT APPLICATION: US/09/823,676 TIME: 07:58:18

Input Set : A:\MBI0034 sequence listing.txt
Output Set: N:\CRF3\04182001\1823676.raw

148 165 170 175	
151 Asn Ala Val Tyr Asp Arg Leu Pro Ile Glu Glu Glu Glu Thr Pro Pro	
152 180 185 190	
155 Pro Arg Thr Thr Gly Val Gln Gln Gln Pro Glu Ala Ser Gln Ser	
156 195 200 205	
159 Ser Glu Val Thr Gly Ser Gly Ala Gln Ala Cys Glu Ser Asn Leu Gln	
160 210 215 220	
163 Gly Gly Asn Gly Gly Gly Val Ala Phe Tyr Asn Leu Gly Met Asn	
164 225 230 235 240	
167 Met Asn Asn Phe Gln Phe Ser Gly Gly Asp Ile Tyr Gly Met Ser Gly	
168 245 250 255	
171 Gly Ser Gly Gly Gly Gly Gly Ala Thr Arg Pro Ala Phe	
172 260 265 270	
175 <210> SEQ ID NO: 3	
176 <211> LENGTH: 1040	
177 <212> TYPE: DNA	
178 <213> ORGANISM: Arabidopsis thaliana	
180 <220> FEATURE:	
181 <221> NAME/KEY: CDS	
182 <222> LOCATION: (82)(879)	
183 <223> OTHER INFORMATION: G2789	
186 <400> SEQUENCE: 3	
187 ctttagggac accaaatcta ttcaacctaa aagcettett tteeeetata ttgaccaact	
189 ttttagcgaa tcagaagagg a atg gat gag gta tct cgt tct cat aca ccg	60
190 Met Asp Glu Val Ser Arg Ser Hig Thr Dro	111
101	
10	
193 caa ttt cta tca agt gat cat cag cac tat cac cat caa aac gct gga	159
194 Gln Phe Leu Ser Ser Asp His Gln His Tyr His His Gln Asn Ala Gly 195 20	
20 23	
197 cga caa aaa cgc ggc aga gaa gaa gga gtt gaa ccc aac aat ata	207
198 Arg Gln Lys Arg Gly Arg Glu Glu Glu Gly Val Glu Pro Asn Asn Ile	
33	
201 ggg gaa gac cta gcc acc ttt cct tcc gga gaa gag aat atc aag aag	255
202 Gly Glu Asp Leu Ala Thr Phe Pro Ser Gly Glu Glu Asn Ile Lys Lys	
203 45 50 55	
205 aga agg cca cgt ggc aga cct gct ggt tcc aag aac aaa ccc aaa gca	303
206 Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys Ala	
207 60 65 70	
209 cca atc ata gtc act cgc gac tcc gcg aac gcc ttc aga tgt cac gtc	351
210 Pro Ile Ile Val Thr Arg Asp Ser Ala Asn Ala Phe Arg Cys His Val	
211 75 80 85 90	
213 atg gag ata acc aac gcc tgc gat gta atg gaa agc cta gcc gtc ttc	399
214 Met Glu Ile Thr Asn Ala Cys Asp Val Met Glu Ser Leu Ala Val Phe	
215 95 100 105	
217 gct aga cgc cgt cag cgt ggc gtt tgc gtc ttg acc gga aac ggg gcc	447
218 Ala Arg Arg Arg Gln Arg Gly Val Cys Val Leu Thr Gly Asn Gly Ala	•
219 110 115 120	
221 gtt aca aac gtc acc gtt aga caa cct ggc gga ggc gtc gtc agt tta	495
222 Val Thr Asn Val Thr Val Arg Gln Pro Gly Gly Gly Val Val Ser Leu	
s1111 Turk Turk Don Don	

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/823,676

DATE: 04/18/2001 TIME: 07:58:18

Input Set : A:\MBI0034 sequence listing.txt
Output Set: N:\CRF3\04182001\I823676.raw

223 125 130 135	
225 cac gga cgg ttt gag att ctt tct ctc tcg ggt tcg ttt ctt cct cc	543
226 His Gly Arg Phe Glu Ile Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro	243
22/ 140 145 150	
229 ccg gca cca cca gct gcg tct ggt tta aag gtt tac tta gcc ggt ggt	591
230 Pro Ala Pro Pro Ala Ala Ser Gly Leu Lys Val Tyr Leu Ala Gly Gly	371
231 155 160 165 170	
233 caa ggt caa gtg atc gga ggc aqt gtg gga ccg ctt acg gca tca	639
234 Gin Gly Gin Val Ile Gly Gly Ser Val Val Gly Pro Leu Thr Ala Ser	037
235 175 180 185	
237 agt ccg gtg gtc gtt atg gca gct tca ttt gga aac gca tct tac gag	687
238 Ser Pro Val Val Met Ala Ala Ser Phe Gly Asn Ala Ser Tyr Glu	007
239 190 195 200	
241 agg ctg cca cta gag gag gag gag act gaa aga gaa ata gat gga	735
242 Arg Leu Pro Leu Glu Glu Glu Glu Glu Thr Glu Arg Glu Ile Asp Gly	, , , ,
243 205 210 215	
245 aac gcg gct agg gcg att gga acg caa acg cag aaa cag tta atg caa	783
246 Asn Ala Ala Arg Ala Ile Gly Thr Gln Thr Gln Lys Gln Leu Met Gln	703
247 220 225 230	
249 gat gcg aca tcg ttt att ggg tcg ccg tcg aat tta att aac tot gtt	831
250 Asp Ala Thr Ser Phe Ile Gly Ser Pro Ser Asn Leu Ile Asn Ser Val	031
251 235 240 245 250	
253 tog ttg coa ggt gaa got tat tgg gga acg caa cga cgg tot tto taa	879
254 Ser Leu Pro Gly Glu Ala Tyr Trp Gly Thr Gln Arg Pro Ser Phe	0/9
²⁵⁵ 255 260 265	
257 gataatatca ttgataatat aagtttcgtc ttcttattct ttttcacttt ttaccttttt	
The same and a segment and the control of the court of the control	939
259 cactitotta ggittigitt taacgittga tiaataccig aaggittitg gaaaattic	939
259 Cacttetta ggttttgttt taacgtttga ttaatacetg aaggtttttg gaaaatttte 261 gateggataa aaggatttat gttgegagee gaaaegegge e	999
259 Cacttetta ggttttgttt taacgtttga ttaatacetg aaggtttttg gaaaatttte 261 gateggataa aaggatttat gttgegagee gaaaegegge c 264 <210> SEQ ID NO: 4	
259 Cacttetta ggittigitt taacgittga ttaatacetg aaggittitig gaaaattite 261 gateggataa aaggattiat gitgegagee gaaaegegge e 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265	999
269 Cacttetta ggttttgttt taacgtttga ttaatacctg aaggtttttg gaaaattttc 261 gatcggataa aaggatttat gttgcgagcc gaaacgcggc c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT	999
261 gateggataa aaggatttat gttgegagee gaaacgegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana	999
261 gateggataa aaggatttat gttgegagee gaaacgegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4	999
261 gateggataa aaggatttat gttgegagee gaaacgegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp	999
261 gateggataa aaggatttat gttgegagee gaaacgegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp 272 1 5 10	999
261 gateggataa aaggatttat gttgegagee gaaacgegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp 272 1 5 10 15 275 His Gln His Tyr His His Gln Asn Ala Gly Arg Gln Lys Arg Gly Arg	999
269 Cacttetta ggttttgttt taacgtttga ttaatacctg aaggtttttg gaaaatttte 261 gateggataa aaggatttat gttgegagee gaaacgegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp 272 1 5 10 15 275 His Gln His Tyr His His Gln Asn Ala Gly Arg Gln Lys Arg Gly Arg 276 20 25 30	999
261 gateggataa aaggatttat gttgegagee gaaacgegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp 272 1 5 10 15 275 His Gln His Tyr His His Gln Asn Ala Gly Arg Gln Lys Arg Gly Arg 276 20 25 30 279 Glu Glu Glu Gly Val Glu Pro Asn Asn Ile Gly Glu Asp Leu Ala Thr	999
261 gateggataa aaggatttat gttgegagee gaaacgegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp 272 1 5 10 15 275 His Gln His Tyr His His Gln Asn Ala Gly Arg Gln Lys Arg Gly Arg 276 20 25 30 279 Glu Glu Glu Gly Val Glu Pro Asn Asn Ile Gly Glu Asp Leu Ala Thr 280 35	999
261 gateggataa aaggatttat gttgegagee gaaacgegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp 272 1 5 10 15 275 His Gln His Tyr His His Gln Asn Ala Gly Arg Gln Lys Arg Gly Arg 276 20 25 30 279 Glu Glu Glu Gly Val Glu Pro Asn Asn Ile Gly Glu Asp Leu Ala Thr 280 35	999
261 gateggataa aaggatttat gttgegagee gaaacgegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp 272 1 5 10 15 275 His Gln His Tyr His His Gln Asn Ala Gly Arg Gln Lys Arg Gly Arg 276 20 25 30 279 Glu Glu Glu Gly Val Glu Pro Asn Asn Ile Gly Glu Asp Leu Ala Thr 280 35 40 45 283 Phe Pro Ser Gly Glu Glu Asn Ile Lys Lys Arg Arg Pro Arg Gly Arg 284 50 55	999
261 gateggataa aaggatttat gttgegagee gaaacgegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp 272 1 5 10 15 275 His Gln His Tyr His His Gln Asn Ala Gly Arg Gln Lys Arg Gly Arg 276 20 25 30 279 Glu Glu Glu Gly Val Glu Pro Asn Asn Ile Gly Glu Asp Leu Ala Thr 280 35 40 45 283 Phe Pro Ser Gly Glu Glu Asn Ile Lys Lys Arg Arg Pro Arg Gly Arg 284 50 55 60 287 Pro Ala Gly Ser Lys Asn Lys Pro Lys Ala Pro Ile Ile Val Thr Arg	999
261 gatcggataa aaggatttat gttgcgagcc gaaacgcggc c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp 272 1	999
259 Cacttetta ggttttgttt taacgtttga ttaatacctg aaggttttg gaaaatttte 261 gateggataa aaggatttat gttgegagee gaaacgegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp 272 1	999
259 Cacttetta ggttttgttt taacgtttga ttaatacctg aaggttttg gaaaatttte 261 gateggataa aaggatttat gttgegagee gaaacgegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp 272 1	999
259 Cacttletta ggttttgttt taacgtttga ttaatacetg aaggtttttg gaaaatttte 261 gateggataa aaggatttat gttgegagee gaaaegegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp 272 1	999
259 Cacttletta ggttttgttt taacgtttga ttaatacetg aaggtttttg gaaaatttte 261 gateggataa aaggatttat gttgegagee gaaaegegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp 272 1	999
261 gatcggataa aaggatttat gttgcgagcc gaaacgcggc c 264 <210 > SEQ ID NO: 4 265 <211 > LENGTH: 265 266 <212 > TYPE: PRT 267 <213 > ORGANISM: Arabidopsis thaliana 269 <400 > SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp 272 1	999
259 Cacttletta ggttttgttt taacgtttga ttaatacetg aaggtttttg gaaaatttte 261 gateggataa aaggatttat gttgegagee gaaaegegge c 264 <210> SEQ ID NO: 4 265 <211> LENGTH: 265 266 <212> TYPE: PRT 267 <213> ORGANISM: Arabidopsis thaliana 269 <400> SEQUENCE: 4 271 Met Asp Glu Val Ser Arg Ser His Thr Pro Gln Phe Leu Ser Ser Asp 272 1	999

RAW SEQUENCE LISTING DATE: 04/18/2001 PATENT APPLICATION: US/09/823,676 TIME: 07:58:18

Input Set : A:\MBI0034 sequence listing.txt
Output Set: N:\CRF3\04182001\1823676.raw

Arg			Gly	Gly	Gly		Val	Ser	Leu	His		Arg	Phe	Glu	Ile	
			Ser	Glv	Ser		Len	Pro	Pro	Pro		Pro	Pro	Δla	Δla	
				1												
		Leu	Lvs	Val		Len	Ala	Glv	Glv		Glv	Gln	Va 1	Tle		
	4 -1		2,0			Dea				Q111	0+1	OIII	141		GLY	
	Ser	Val	Val			Leu	Thr	Ala		Ser	Pro	Va l	Va 1		Met	
			180	4								,				
Ala	Ala	Ser	Phe	Gly	Asn	Ala	Ser		Glu	Ara	Leu	Pro		Glu	Glu	
		195		-			200	-1-		5					010	
Glu	Glu	Glu	Thr	Glu	Arq	Glu		Asp	Gly	Asn	Ala		Arg	Ala	Ile	
	210				•	215		•	_		220		,			
Gly	Thr	Gln	Thr	Gln	Lys	Gln	Leu	Met	Gln	Asp	Ala	Thr	Ser	Phe	Ile	
					230					235					240	
Gly	Ser	Pro	Ser	Asn	Leu	Ile	Asn	Ser	Val	Ser	Leu	Pro	Gly	Glu	Ala	
				245					250				-	255		
Tyr	Trp	Gly	Thr	Gln	Arg	Pro	Ser	Phe								
			260					265								
<210	0> S	EQ II	ON C	: 5												
<21	1> L	ENGTI	H: 13	L30												
<212	2> T	YPE:	DNA													
<213	3> O	RGAN	SM:	Aral	oidor	sis	thal	liana	a .							
<220	0> F1	EATUI	RE:													
<22	1> N	AME/I	KEY:	CDS												
<222	2> L((189	9)((1019)									
<222 <223		OCAT:	ON:													
<223 <400	3> 0: 0> SI	OCATI THER EQUEI	ON: INFO ICE:	ORMAT 5	CION:	G19	945									
<223 <400 att	3> 0: 0> SI tecea	CATI THER EQUEI aaa g	ON: INFO ICE: Jggat	ORMAN 5 ttac	rion:	: G19 aagt	945 ccct								occata	60
<223 <400 atti	3> 0' 0> Si tecea acaa	OCATI THER EQUEN aaa g	ON: INFO ICE: Iggat	ORMAT 5 ttac itctt	rion: eg aa cc tt	G19 aagt	945 ccct cttct	tcc	ctcct	ctt	ttat	tttc	tt t	ttaa	aatcat	60 120
<223 <400 atti ccaa ttao	3> 05 0> Si tecea acaa cacaa	DCATI THER EQUEN aaa g cct c	ION: INFO NCE: gggat ctaca itcca	ORMAT 5 ttac itctt iaaga	rion: eg aa to tt ac aa	G19 aagt cttc	945 ccct cttct cgaaa	tct tct	ctcct	ctt	ttat acaa	tttc	tt t	ttaa aaaat	atcat taagaa	
<223 <400 atti ccaa ttao	3> 05 0> Si tecea acaa cacaa	OCATI THER EQUEN aaa g cct o	ION: INFO NCE: jggat ctaca itcca j aaa	ORMAT 5 ttac itcti iaaga i ggt	rion: eg aa cctt acaa gaa	aagt cttc atct	045 ccct cttct cgaaa c aga	tct tct gag	ctcct ctaa g caa	ctt itaa i aag	ttat acaa agt	tttc atco aac	tt t at a gaa	ttaa aaat aat	aatcat aagaa g ttt	120
<223 <400 atti ccaa ttao	3> 05 0> Si tecea acaa cacaa	OCATI THER EQUEN CCT C C CCT C C CCT C C C C	ION: INFO NCE: jggat ctaca itcca j aaa	ORMAT 5 ttac itcti iaaga i ggt	rion: eg aa cc tt ac aa gaa	G19 aagt cttc atct tact tac	045 ccct cttct cgaaa c aga	tct tct gag	ctcct ctaa g caa	ctt itaa i aag	ttat acaa agt	tttc atco aac	tt t at a gaa	ttaa aaat aat	atcat taagaa	120 180
<223 <400 atti ccas ttac aaac	3> 05 0> SI teces acaas cacas caaas	OCATI THER EQUEN aaa g cct c aaa a g atg Met	ION: INFO NCE: gggat ctaca itcca g aaa Lys	ORMAN 5 ttac itctt iaaga i ggt	rion: eg aa cctt ac aa gaa gaa	G19 naagt cette natet n tac n Tyr	ecct ettet egaaa e aga	tco tct gag g Glu	ctcct ctaa g caa g Glr	ctt itaa i aag i Lys	ttat acaa agt Ser 10	tttto atco aac Asn	ett t eat a e gaa e Glu	ttaa aaaat aatg Met	aatcat caagaa g ttt : Phe	120 180
<223 <400 atti ccaa ttac aaac tcc	3> 05 D> SI tecea acaac cacaa cacaa	DCATI THER EQUEN aaa g cct caaa a g atg Met 1 ctt	ION: INFO NCE: Jggat etaca tcca tcca Lys	DRMAT 5 tttac itcti iaaga i ggt i Gly	rion: cg aa cc tt cc aa cgaa cat cat	aaagt cetto aatet tac Tyr 5	945 cccct cttct cgaaa c aga c Arg	tco tct gag g Glu	ctcct ctaa g caa g Glr cag	ctt itaa i aag i Lys caa	ttat acaa agt Ser 10 caa	atco acc acc Asn	ett t eat a e gaa e Glu	ttaa aaaat a atg 1 Met	aatcat caagaa g ttt : Phe caa	120 180
<223 <400 atti ccas ttac aaac tcc Ser	3> 05 D> SI tecea acaac cacaa cacaa	DCATI THER EQUEN aaa g cct caaa a g atg Met 1 ctt	ION: INFO NCE: Jggat etaca tcca tcca Lys	DRMAT 5 tttac itcti iaaga i ggt i Gly	rion: cg aa cc tt ac aa cgaa cat His	aaagt cetto aatet tac Tyr 5	945 cccct cttct cgaaa c aga c Arg	tco tct gag g Glu	ctcct ctaa g caa g Glr cag	ctt itaa i aag i Lys caa Gln	ttat acaa agt Ser 10 caa	atco acc acc Asn	ett t eat a e gaa e Glu	ttaa aaaat a atg 1 Met	aatcat caagaa g ttt : Phe caa Gln	120 180 230
<223 <400 atti ccas ttac aaac tcc Ser 15	3> 07 D> SI tccca acaac cacaa cacaa caaaa caaaa taag Lys	OCATI THER EQUEN aaa coct of aaa a g ato Met 1 ctt Leu	ION: INFO NCE: jggat ctaca itcca j aaa Lys cct Pro	DRMAT 5 cttac itcti aaaga ggt Gly cat His	rion: cg aa cc tt c gaa r Glu cat His 20	aagt cette atet tac Tyr 5 caa Gln	ettet ettet egaaa e aga e Arg caa Gln	tco tct gag g Glu caa Gln	ctcct cctaa g caa i Glr cag Gln	ctt itaa i aag i Lys caa Gln 25	ttat acaa agt Ser 10 caa Gln	ttto atco aac Asn caa Gln	ett teat a e gaa e Glu caa Gln	ttaa aaaat aato Met caa Gln	aatcat caagaa g ttt : Phe caa Gln 30	120 180 230 278
<223 <400 atti ccaa ttac aaac tcc Ser 15 cac	3> 07 D> SI tccca acaac caaac caaac caaac taaag Lys tct	CCATI THER EQUEN aaa g cct caaa a g atg Met 1 ctt Leu	ION: INFO INFO ICE: INFO ICE: INFO ICE	DRMAT 5 cttac itcti aaaga ggt Gly cat His	rion: cg aa cc tt ac aa r gaa r Glu cat His 20 cac	aagt cette atet tac Tyr 5 caa Gln	ettet egaaa e aga e Arg caa Gln	tec tet gag g Glu caa Gln	ctcct cctaa g caa g caa Glr cag Gln	caa Gln 25 tcc	ttat acaa g agt s Ser 10 caa Gln	atco aac Asn caa Gln	ett teat a gaa a Glucaa Glucaa Glucaa acc	ttaa aaaat a atg n Met caa Gln	aatcat caagaa g ttt : Phe caa Gln 30 acc	120 180 230
<223 <400 atti ccas ttac aaac tcc Ser 15	3> 07 D> SI tccca acaac caaac caaac caaac taaac tys	CCATI THER EQUEN aaa g cct caaa a g atg Met 1 ctt Leu	ION: INFO INFO ICE: INFO ICE: INFO ICE	DRMAN 5 cttac itcti aaaga ggt Gly cat His tct Ser	rion: cg aa cc tt ac aa r gaa r Glu cat His 20 cac	aagt cette atet tac Tyr 5 caa Gln	ettet egaaa e aga e Arg caa Gln	tec tet gag g Glu caa Gln	ctect cctaa g caa g Car cag Gln tcc Ser	caa Gln 25 tcc	ttat acaa g agt s Ser 10 caa Gln	atco aac Asn caa Gln	ett teat a gaa a Glucaa Glucaa Glucaa acc	cttaa aaaat a atg Caa Gln ccc Pro	aatcat caagaa g ttt : Phe caa Gln 30 acc	120 180 230 278
<223 <400 atti ccas ttac aaac tcc Ser 15 cac His	3> 00 0> SI tccca acaac caaac aaag Lys tct Ser	CCATI THER EQUEN aaa g cct caaa a g ato Met 1 ctt Leu ctt	ION: INFO INFO ICE: Joggat Loca Loca Lys Cct Pro acc Thr	DRMAN 5 cttac cttac caaga cgt cat His tct Ser 35	cg aac ttac aac gaac Glucat His	aagt cette atet tact Tyr 5 caa Gln tte	cect cttct cgaaa c aga c Arg caa Gln cac	tection tectio	ctect cctaa g caa g Clr cag Gln tcc Ser 40	caa Gln 25 tcc Ser	ttat acaa gagt Ser 10 caa Gln acc Thr	ttto atco aac Asn caa Gln gta Val	ett teat a gaa Glucaa G	caa Gln ccc Pro 45	aatcat caagaa g ttt : Phe caa Gln 30 acc Thr	120 180 230 278 326
<223 <400 atti ccas ttac aaac tcc Ser 15 cac His	3> 00 0> SI tccca acaa acaa aag Lys tct Ser	CCATI THER EQUEN aaa g cct caaa a g ato Met 1 ctt Leu ctt Leu	ION: INFO INFO INFO INFO INFO INFO INFO INFO	DRMAN 5 cttac cttac caaga cgt cat His tct Ser 35 tcc	rion: eg aa cc tt cat His cac His cac His cac dac dac dac dac dac dac da	aaagt cette atet tact Tyr 5 caa Gln ttc Phe	045 teect tettet tgaaa caaga caa Gln cac His	tct tct gag Glu caa Gln ctc Leu	ctcct cctaa g caa g Clr cag Gln tcc Ser 40 cga	caa Gln 25 tcc Ser	ttat acaa gagt Ser 10 caa Gln acc Thr	atco acca Asn caa Gln gta Val	ett teat a e gaa e Glu caa Gln acc Thr	caa Gln ccc Pro 45 aga	aatcat caagaa g ttt : Phe caa Gln 30 acc Thr	120 180 230 278
<223 <400 atti ccas ttac aaac tcc Ser 15 cac His	3> 00 0> SI tccca acaa acaa aag Lys tct Ser	CCATI THER EQUEN aaa g cct caaa a g ato Met 1 ctt Leu ctt Leu	ION: INFO NCE: gggat stace stace stace tcca cct Pro acc Thr tcc Ser	DRMAN 5 cttac cttac caaga cgt cat His tct Ser 35 tcc	rion: eg aa cc tt cat His cac His cac His cac dac dac dac dac dac dac da	aaagt cette atet tact Tyr 5 caa Gln ttc Phe	045 teect tettet tgaaa caaga caa Gln cac His	t too t tot gag g Glu caa Gln ctc Leu gtc	ctcct cctaa g caa g Clr cag Gln tcc Ser 40 cga	caa Gln 25 tcc Ser	ttat acaa gagt Ser 10 caa Gln acc Thr	atco acca Asn caa Gln gta Val	ett teat a e gaa e Glu caa Gln acc Thr ggc Gly	caa Gln ccc Pro 45 aga	aatcat caagaa g ttt : Phe caa Gln 30 acc Thr	120 180 230 278 326
<223 <400 atti ccas ttac aaac tcc Ser 15 cac His gtc Val	3> 00 0> Si tccca acaaa caaaa Lys tct Ser gat Asp	CCATI THER EQUEN aaa g cct caaa a g atg Met 1 ctt Leu ctt Leu gac Asp	ION: INFO NCE: gggat tcca tcca tcca tcca tcca tcca tcc	DRMAN 5 cttac atctt aaaga cgt Gly cat His tct Ser 35 tcc Ser	eg aace ttac aac gaac Glucat His 20 cac His atc Ile	aaagt cette atet tac Tyr 5 caa Gln tte Phe gaa Glu	ecct cttct cgaaa cagaaa caa Caa Gln cac His gtg	caa Gln ctc gtc Val	ctect cctaa g caa g caa cag Gln tcc Ser 40 cga Arg	cat a aag a Lys caa Gln 25 tcc Ser cgt Arg	ttat acaa agt Ser 10 caa Gln acc Thr	caa Gln gta Val	ett teat a caa Gln acc Thr Ggc Gly 60	cttaa aaaat a atg n Met caa Gln ccc Pro 45 aga Arg	aatcat caagaa g ttt Phe caa Gln 30 acc Thr cca	120 180 230 278 326
<223 <400 atti ccaa ttac aaac tcc Ser 15 cac His gtc Val	3> 00 0> Si tccca acaaa caaaa Lys tct Ser gat Asp	CCATI THER EQUEN aaa g cct caaa a g atg Met 1 ctt Leu ctt Leu gac Asp	ION: INFO NCE: gggat tcca g aaa Lys cct Pro acc Thr tcc Ser 50 aaa	DRMAN 5 cttac itcti iaaga i ggt cat His tct Ser 35 tcc Ser aac	eg aace ttac aac gaar Glucat His 20 cac His atc Ile	aaagt cette atet tac Tyr 5 caa Gln ttc Phe gaa Glu	od5 ccct cgaaa cagaaa cagaaa caa Gln cac His gtg Val	caa Gln ctc Leu gtc Val 55 cca	ctect cctaa g caa g caa g Gln tcc Ser 40 cga Arg	catt a aag a Lys caa Gln 25 tcc Ser cgt Arg	ttat acaa g agt s Ser 10 caa Gln acc Thr cca Pro	caa Gln gta Val cgt Arg	cat de gaa Glucaa Gluca	cttaa aaaat a atg 1 Met caa Gln ccc Pro 45 aga Arg	aatcat caagaa g ttt cPhe caa Gln 30 acc Thr cca Pro	120 180 230 278 326
<223 <400 atti ccas ttac aaac tcc Ser 15 cac His gtc Val	3> 00 0> Si tccca acaaa caaaa Lys tct Ser gat Asp	CCATI THER EQUEN aaa g cct caaa a g ate 1 ctt Leu ctt Leu gac Asp tcc	ION: INFO NCE: gggat tcca g aaa Lys cct Pro acc Thr tcc Ser 50 aaa	DRMAN 5 cttac itcti iaaga i ggt cat His tct Ser 35 tcc Ser aac	eg aace ttac aac gaar Glucat His 20 cac His atc Ile	aaagt cette atet tact Tyr 5 caa Gln ttc Phe gaa Glu cct	ecct ettet egaaa e aga e Arg caa Gln cac His gtg Val aaa Lys	caa Gln ctc Leu gtc Val 55 cca	ctect cctaa g caa g caa g Gln tcc Ser 40 cga Arg	catt a aag a Lys caa Gln 25 tcc Ser cgt Arg	ttat acaa g agt Ser 10 caa Gln acc Thr cca Pro	caa Gln gta Val cgt Arg	cat de gaa Glucaa Gluca	cttaa aaaat a atg 1 Met caa Gln ccc Pro 45 aga Arg	aatcat caagaa g ttt cPhe caa Gln 30 acc Thr cca Pro	120 180 230 278 326
<223 <400 atti ccas ttac aaac tcc Ser 15 cac His gtc Val cca Pro	3> Office of the control of the cont	CCATIFIER EQUENTED AND A COLOR OF	ION: INFO NCE: INFO ICE: INFO INFO ICE: INFO INFO ICE: INFO ICE: INFO ICE: INFO ICE: INFO ICE: INFO ICE: INFO INFO ICE: INFO INFO ICE: INFO ICE: INFO ICE: INFO ICE: INFO ICE: INFO ICE: INFO INFO INFO INFO INFO INFO INFO INFO	DRMAN 5 cttac itett inagga i ggt i Gly cat His tet Ser 35 tec Ser aac Asn	eg aace ttac aac gaac Glucat His 20 cac His atc Ile aaa Lys	aaagt cette atet tact Tyr 5 caa Gln ttc Phe gaa Glu cct	ccct cttct cgaaa cagaaa caa Gln cac His gtg Val aaa Lys	caa Gln ctc y Glu caa Gln ctc Leu gtc Val 55 cca Pro	ctect cctas g cas g cas g cas Gln tcc Ser 40 cga Arg	catt a aag a Lys caa Gln 25 tcc Ser cgt Arg	ttat acaa g agt Ser 10 caa Gln acc Thr cca Pro	caa Gln gta Val cgt Arg gtc Val 75	caa Gln acc Thr Ggc Gly 60 aca Thr	caa Gln ccc Pro 45 aga Arg	aatcat caagaa g ttt Phe caa Gln 30 acc Thr cca Pro gac Asp	120 180 230 278 326 374
<223 <400 atti ccaa ttac aaac tcc Ser 15 cac His gtc Val cca Pro acc	3> Office of the control of the cont	CCATIFIER EQUENTED AND A COLOR OF	ON: INFO INFO INFO INFO INFO INFO INFO INFO	DRMAN 5 cttac itett inagga i ggt i Gly cat His tet Ser 35 tec Ser aac Asn atg	eg aace ttac aac gaac Glucat His 20 cac His atc Ile aaa Lys	aaagt cette atet tact Tyr caa Gln ttc Phe gaa Glu cet	ccct cttct cgaaa cagaaa caa Gln cac His gtg Val aaa Lys 70 tac	caa Gln ctc Leu gtc Val 55 cca Pro atc	ctcct cctaa g caa g caa g Gln cag Gln tcc Ser 40 cga Arg ccc Pro	cctt itaa i aag i Lys caa Gln 25 tcc Ser cgt Arg gtc Val	ttat acaa g agt Ser 10 caa Gln acc Thr cca Pro ttc	caa Gln gta Val cgt Arg gtc Val 75	ett teat a se gaa a Glu caa Glu acc Thr ggc Gly aca Thr tca	cttaa aaaat a atg 1 Met caa Gln ccc Pro 45 aga Arg cgt Arg	aatcat caagaa g ttt Phe caa Gln 30 acc Thr cca Pro gac Asp	120 180 230 278 326
<223 <400 atti ccas ttac aaac tcc Ser 15 cac His gtc Val cca Pro	3> Office of the control of the cont	CCATIFIER EQUENTED AND A COLOR OF	ON: INFO INFO INFO INFO INFO INFO INFO INFO	DRMAN 5 cttac itett inagga i ggt i Gly cat His tet Ser 35 tec Ser aac Asn atg	eg aace ttac aac gaac Glucat His 20 cac His atc Ile aaa Lys	aaagt cette atet tact Tyr caa Gln ttc Phe gaa Glu cct Pro	ccct cttct cgaaa cagaaa caa Gln cac His gtg Val aaa Lys 70 tac	caa Gln ctc Leu gtc Val 55 cca Pro atc	ctcct cctaa g caa g caa g Gln cag Gln tcc Ser 40 cga Arg ccc Pro	cett itaa i aag i Lys caa Gln 25 tee Ser cgt Arg gte Val gaa Glu	ttat acaa g agt Ser 10 caa Gln acc Thr cca Pro ttc Phe gtt Val	caa Gln gta Val cgt Arg gtc Val 75	ett teat a se gaa a Glu caa Glu acc Thr ggc Gly aca Thr tca	cttaa aaaat a atg 1 Met caa Gln ccc Pro 45 aga Arg cgt Arg	aatcat caagaa g ttt Phe caa Gln 30 acc Thr cca Pro gac Asp	120 180 230 278 326 374
<223 <400 atti ccaa ttac aaac tcc Ser 15 cac His gtc Val cca Pro acc	3> Office of the control of the cont	CCATIFIER EQUENTED AT A COLOR OF	ION: INFO NCE: INFO INFO INFO INFO INFO INFO INFO INFO	DRMAN 5 cttac itetti aaaga i ggt i Gly cat His tet Ser 35 tec Ser aac Asn atg	cg aacc ttac aac gaaa cat His 20 cac His atc Ile aaa Lys agt Ser	aaagt cetto atet tact Tyr caa Gln ttc Phe gaa Glu cct Pro	ccct cttct cgaaa caga caa Gln cac His yal aaa Lys 70 tac	caa Gln ctc Leu gtc Val 55 cca Pro atc Ile	ctcct cctaa g caa g caa g Cln cag Gln tcc Ser 40 cga Arg ccc Pro ctc Leu	cctt itaa i aag i Lys caa Gln 25 tcc Ser cgt Arg gtc Val gaa Glu	ttat acaa g agt Ser 10 caa Gln acc Thr cca Pro ttc Phe gtt Val 90	caa Gln gta Val cgt Arg gtc Pro	ett teat a gaaa gloon gala gala gala gala gala gala gala gal	tttaa aaaat a atc caa Gln ccc Pro 45 aga Arg cgt Arg gga Gly	aatcat caagaa g ttt cPhe caa Gln 30 acc Thr cca Pro gac Asp aac Asn	120 180 230 278 326 374
	Leu 145 Ser Gly Ala Glu Gly 225 Gly Tyr <210 <211 <211 <221	130 Leu Ser 145 Ser Gly Gly Ser Ala Ala Glu Glu 210 Gly Thr 225 Gly Ser Tyr Trp <210> Si <211> Li <212> Ti <213> Oi <220> Fi	130 Leu Ser Leu 145 Ser Gly Leu Gly Ser Val Ala Ala Ser 195 Glu Glu Glu 210 Gly Thr Gln 225 Gly Ser Pro Tyr Trp Gly <210> SEQ II <211> LENGTH <212> TYPE: <213> ORGANI <220> FEATUR	130 Leu Ser Leu Ser 145 Ser Gly Leu Lys Gly Ser Val Val 180 Ala Ala Ser Phe 195 Glu Glu Glu Thr 210 Gly Thr Gln Thr 225 Gly Ser Pro Ser Tyr Trp Gly Thr 260 <210> SEQ ID NO <211> LENGTH: 13 <212> TYPE: DNA <213> ORGANISM: <220> FEATURE:	130 Leu Ser Leu Ser Gly 145 Ser Gly Leu Lys Val 165 Gly Ser Val Val Gly 180 Ala Ala Ser Phe Gly 195 Glu Glu Glu Thr Glu 210 Gly Thr Gln Thr Gln 225 Gly Ser Pro Ser Asn 245 Tyr Trp Gly Thr Gln 260 <210> SEQ ID NO: 5 <211> LENGTH: 1130 <212> TYPE: DNA <213> ORGANISM: Arab	130 Leu Ser Leu Ser Gly Ser 145 Ser Gly Leu Lys Val Tyr 165 Gly Ser Val Val Gly Pro 180 Ala Ala Ser Phe Gly Asn 195 Glu Glu Glu Thr Glu Arg 210 Gly Thr Gln Thr Gln Lys 225 Tyr Trp Gly Thr Gln Arg 260 <210> SEQ ID NO: 5 <211> LENGTH: 1130 <212> TYPE: DNA <213> ORGANISM: Arabidor 220> FEATURE:	130	130 Leu Ser Leu Ser Gly Ser Phe Leu 145 Ser Gly Leu Lys Val Tyr Leu Ala 165 Gly Ser Val Val Gly Pro Leu Thr 180 Ala Ala Ser Phe Gly Asn Ala Ser 195 Glu Glu Glu Thr Glu Arg Glu Ile 210 Gly Thr Gln Thr Gln Lys Gln Leu 225 Gly Ser Pro Ser Asn Leu Ile Asn 245 Tyr Trp Gly Thr Gln Arg Pro Ser 260 <210> SEQ ID NO: 5 <211> LENGTH: 1130 <212> TYPE: DNA <220> FEATURE:	130	130	130	130	130	130	Leu Ser Leu Ser Gly Ser Phe Leu Pro Pro Pro Ala Pro Pro Ala 145 150 155 155 155 165 165 165 165 170 175 175 175 175 175 175 175 175 175 175 175 175 180	Leu Ser Leu Ser Cly Ser Phe Leu Pro Pro Pro Ala Pro Pro Ala Ala 145

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/823,676

DATE: 04/18/2001

TIME: 07:58:19

Input Set : A:\MBI0034 sequence listing.txt
Output Set: N:\CRF3\04182001\1823676.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date